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☐ 1: NP_660187. ATP-binding casse...[gi:21729876]

BLink, Domains, Links

LOCUS NP_660187 1344 aa linear PRI 07-SEP-2003
DEFINITION ATP-binding cassette, sub-family C, member 11 isoform b;
multi-resistance protein 8; ATP-binding cassette transporter MRP8;
ATP-binding cassette protein C11 [Homo sapiens].
ACCESSION NP_660187
VERSION NP_660187.1 GI:21729876
DBSOURCE REFSEQ: accession [NM_145186.1](#)
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 1344)
AUTHORS Turriziani, O., Schuetz, J.D., Focher, F., Scagnolari, C., Sampath, J.,
Adachi, M., Bambacioni, F., Riva, E. and Antonelli, G.
TITLE Impaired 2',3'-dideoxy-3'-thiacytidine accumulation in
T-lymphoblastoid cells as a mechanism of acquired resistance
independent of multidrug resistant protein 4 with a possible role
for ATP-binding cassette C11
JOURNAL Biochem. J. 368 (Pt 1), 325-332 (2002)
MEDLINE 22304623
PUBMED 12133003
REMARK GeneRIF: Impaired 2',3'-dideoxy-3'-thiacytidine accumulation in
T-lymphoblastoid cells as a mechanism of acquired resistance
independent of multidrug resistant protein 4 with a possible role
for ATP-binding cassette C11.
REFERENCE 2 (residues 1 to 1344)
AUTHORS Yabuuchi, H., Shimizu, H., Takayanagi, S. and Ishikawa, T.
TITLE Multiple splicing variants of two new human ATP-binding cassette
transporters, ABCC11 and ABCC12
JOURNAL Biochem. Biophys. Res. Commun. 288 (4), 933-939 (2001)
MEDLINE 21547789
PUBMED 11688999
REMARK GeneRIF: alternative splice variants and gene expression
REFERENCE 3 (residues 1 to 1344)
AUTHORS Bera, T.K., Lee, S., Salvatore, G., Lee, B. and Pastan, I.
TITLE MRP8, a new member of ABC transporter superfamily, identified by
EST database mining and gene prediction program, is highly
expressed in breast cancer
JOURNAL Mol. Med. 7 (8), 509-516 (2001)
MEDLINE 21475973
PUBMED 11591886
REFERENCE 4 (residues 1 to 1344)
AUTHORS Tammur, J., Prades, C., Arnould, I., Rzhetsky, A., Hutchinson, A.,
Adachi, M., Schuetz, J.D., Swoboda, K.J., Ptacek, L.J., Rosier, M.,
Dean, M. and Allikmets, R.
TITLE Two new genes from the human ATP-binding cassette transporter

superfamily, ABCC11 and ABCC12, tandemly duplicated on chromosome 16q12

JOURNAL Gene 273 (1), 89-96 (2001)
 MEDLINE [21376129](#)
 PUBMED [11483364](#)

REFERENCE 5 (residues 1 to 1344)
 AUTHORS Dean,M., Rzhetsky,A. and Allikmets,R.
 TITLE The human ATP-binding cassette (ABC) transporter superfamily
 JOURNAL Genome Res. 11 (7), 1156-1166 (2001)
 MEDLINE [21329047](#)
 PUBMED [11435397](#)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [AF411579.1](#).

Summary: The protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABCC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This ABC full transporter is a member of the MRP subfamily which is involved in multi-drug resistance. It is expressed at low levels in all tissues, except kidney, spleen, and colon. This gene and family member ABCC12 are determined to be derived by duplication and are both localized to chromosome 16q12.1. Their chromosomal localization, potential function, and expression patterns identify them as candidates for paroxysmal kinesigenic choreoathetosis, a disorder characterized by attacks of involuntary movements and postures, chorea, and dystonia. Multiple alternatively spliced transcript variants have been described for this gene.

Transcript Variant: This variant (3) lacks an alternate in-frame exon compared to variant 1, resulting in a shorter protein (isoform b), compared to isoform a.

FEATURES

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 /chromosome="16"
 /map="16q12.1"

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 /note="MdlB"
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Region 853..1338
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 /db_xref="LocusID:85320"
 /db_xref="MIM:607040"

ORIGIN

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181 piliipkile yseeqlgnvv hgvglcalf lsecvkslsf ssswiinqrt airfraavss
241 fafekliqfk svihitsgea isfftgdvny lfegvcygp1 vlitcaslvi csissyfiig
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421 laslnllrls vffvpiavkg ltnsksavmr fkkfflqesp vfyvqtlqdp skalvfeeat
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721 qkkgkyaqli qkmhkeatsd mlqdtakiae kpkvesqala tsleeslgn avpehqltqe
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841 resngtmadl gniadnpqls fyqlvyglna lllicvgvcs sgiftkvtrk astalhnklf
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1261 ilideatasi dmetdtliqr tireafqgct vlviahrvtt vlncdhilvm gngkvvefdr
1321 pevlrkkpgs lfaalmatat sslr

//

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Sep 4 2003 10:24:36

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

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>seqid24
vs /tmp/fastaHAACJayWj library
searching /tmp/fastaHAACJayWj library

1344 residues in 1 sequences

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join: 40, opt: 28, gap-pen: -12/-2, width: 16
Scan time: 0.034

The best scores are: opt

NP_660187 ACCESSION:NP_660187 NID: gi 21729876 re (1344) 4838

>>NP_660187 ACCESSION:NP_660187 NID: gi 21729876 ref NP_ (1344 aa)

initn: 7156 initl: 4838 opt: 4838

Smith-Waterman score: 7274; 85.311% identity in 1382 aa overlap (1-1219:1-1344)

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NP_660 LR